

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions and listings of claims in the application:

1. (Currently amended) A method of identifying a cell, tissue or nucleus, comprising:

obtaining a ~~analyzing the~~ DNA methylation pattern for ~~of~~ the cell, tissue or nucleus;

obtaining a ~~analyzing the~~ DNA methylation pattern for ~~of~~ one or more known types of ~~the~~ cell, tissue or nucleus; and, ~~and~~;

comparing the DNA methylation pattern of the cell, tissue or nucleus with the DNA methylation pattern of the one or more known types of cell, tissue or nucleus, thereby identifying the cell, tissue or nucleus.

2. (Canceled)

3. (Canceled)

4. (Withdrawn) A computer-readable record medium in which a program that permits a computer to function as an identification system for cells, tissues or nuclei has been recorded, said identification system comprising:

(a) means for analyzing information on the methylation pattern of DNA isolated from a test cell, tissue or nucleus; and

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(b) means for identifying the cell, tissue or nucleus using the analysis results as an indicator.

5. (Currently amended) A method of assessing the differentiation state development of a ~~certain type of~~ cell, tissue or nucleus comprising:

~~obtaining a identifying the DNA methylation pattern for the of one or more known types of cell, tissue or nucleus, and;~~

~~obtaining a identifying the DNA methylation pattern of an unknown for one or more cell, tissue or nucleus of known differentiation state; and, and;~~

~~comparing the DNA methylation pattern of the one or more known types of cell, tissue or nucleus with the DNA methylation pattern of the unknown cell, tissue or nucleus with the DNA methylation pattern of the one or more cell, tissue or nucleus of known differentiation state, to determine whether the unknown cell, tissue or nucleus has the same DNA methylation pattern as the one or more known types of cell, tissue or nucleus, thereby assessing the differentiation state of the cell, tissue or nucleus determining whether the certain type of cell, tissue or nucleus is present.~~

6. (New) The method of claim 5, wherein the DNA methylation patterns each comprise at least about 1,000 gene regions.

7. (New) The method of claim 5, further comprising identifying the methylated and demethylated gene regions that specify the differentiation state of the cell, tissue, or nucleus.

8. (New) The method of claim 5, wherein the cell, tissue, or nucleus is a stem cell.
9. (New) The method of claim 5, wherein the DNA methylation patterns are analyzed by generating RLGS profiles.
10. (New) The method of claim 1, wherein the DNA methylation patterns each comprise at least about 1,000 gene regions.
11. (New) The method of claim 1, further comprising identifying the methylated and demethylated gene regions that specify the identity of the cell, tissue, or nucleus.
12. (New) The method of claim 1, wherein the cell, tissue, or nucleus is a stem cell.
13. (New) The method of claim 1, wherein the DNA methylation patterns are analyzed by generating RLGS profiles.
14. (New) A method of producing a differentiated cell, tissue, or nucleus comprising:
- methylating or demethylating the gene regions identified by the method of claim 7 in a cell, tissue, or nucleus, so as to specify a desired differentiation state; and
- producing a differentiated cell, tissue, or nucleus.